ESTRUCTURA DE MACROMOLECULAS
Programa de seminarios del curso 2025-2026

EQUIPO	SEMINARIO ESCOGIDO	Día
María Millán Anna Gallego Andrea Lamata Lucía Bas	Salillas etal (2021) ***Selective targeting of human and animal pathogens of the Helicobacter genus by flavodoxin inhibitors: efficacy, synergy, resistance, and mechanistic studies***	24 N
Alejandro Alquezar Cañas Pablo Daniel Martínez García Sara Cortes Cubero Catalina Jerez Losa	Galano-Frutosetal (2024) ***L-Thyroxine and L-thyroxine-based antimicrobials against Streptococcus pneumoniae and other Gram-positive bacteria***	24 N
David Alija Paula Martínez Adiego Marta Monserrate Lucas Gascón Zurita	Conde-Giménez etal (2022) ***Alchemical Design of Pharmacological Chaperones with higher Affinity for Phenylalanine Hydroxylase***	25 N
Iker Cortés Nader Zapata Kaitlyn Ramón Eva Valero	Alonso etal (2024).pdf ***Association between missense variants of uncertain significance in the CHEK2 gene and hereditary breast cancer: a cosegregation and bioinformatics analysis***	25 N
Pablo Cartañá Polo Iván Nogués Jové Massimo García Olivares Daniel Torres Toro	Galano-Frutoset al2022 ***A look at the face of the molten globule: structural model of the Helicobacter pylori apoflavodoxin ensemble at acidic pH***	26 N
Marina Ramón Igea Aimara Cuartielles Zalba Sofía Martínez Cuartero Rocío Mañas Sicilia	García-Cebollada etal (2022) ***Protposer: the web server that readily proposes protein stabilizing mutations with high PPV***	26 N
Violeta Serrano Gracia Juan Moreno Muñoz Martina Luzán Barrabés Rubén Hernández Barón	Galano-Frutos etal (2021) ***Molecular Dynamics Simulations for Genetic Interpretation in Protein Coding Regions: Where we Are, Where to Go and When***	1D
Marina Salillas Rodés Verónica Martínez Luzón Andrea Esteban Blasco Inés Valiente Herrero	Conde-Jiménez & Sancho(2021) ***Unravelling the Complex Denaturant and Thermal-Induced Unfolding Equilibria of Human Phenylalanine Hydroxylase***	1D
Mario Iranzo Marina Pérez Marina Gimeno Pilar Gaspar	Lamazares etal (2015) ***Rational stabilization of complex proteins: a divide and combine approach***	2D
Lucía Castillo Peña Alejandra Bartolomé Serrano Andrea Megino Hernández Naiara Aragón Doiz	Galano-Frutos&Sancho(2024) ***Energy, water, and protein folding: A molecular dynamics based quantitative inventory of molecular interactions and forces that make proteins stable***	2D
Diana Los Gómez Natalia Martín Colell Nuria Mauleón Laura Casado Puche	Helena García-Cebollada et al. (2025) ***ProteinLIPs: a web server for identifying highly polar and poorly packed interfaces in proteins***	3D